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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/075,987

DATE: 05/07/2002

TIME: 11:47:07

Input Set : N:\Crf3\RULE60\10075987.raw

Output Set: N:\CRF3\05072002\J075987.raw

1 <110> APPLICANT: Glucksmann, Maria A.
2 <120> TITLE OF INVENTION: 14273 Receptor, A Novel G-Protein Coupled Receptor
3 <130> FILE REFERENCE: 5800-4B, 035800/17086
4 <140> CURRENT APPLICATION NUMBER: 10/075,987
5 <141> CURRENT FILING DATE: 2002-02-13
6 <150> PRIOR APPLICATION NUMBER: US/09/261,599B
7 <151> PRIOR FILING DATE: 1999-02-26
8 <150> PRIOR APPLICATION NUMBER: 09/223,538
9 <151> PRIOR FILING DATE: 1998-12-30
10 <160> NUMBER OF SEQ ID NOS: 7
11 <170> SOFTWARE: PatentIn Ver. 2.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 361
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens
17 <400> SEQUENCE: 1

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20	Leu	Glu	Gln	Ala	Asn	Arg	Thr	Arg	Phe	Pro	Phe	Phe	Ser	Asp	Val	Lys
21				20					25					30		
22	Gly	Asp	His	Arg	Leu	Val	Leu	Ala	Ala	Val	Glu	Thr	Thr	Val	Leu	Val
23			35					40					45			
24	Leu	Ile	Phe	Ala	Val	Ser	Leu	Gly	Asn	Val	Cys	Ala	Leu	Val	Leu	
25	50						55				60					
26	Val	Ala	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Thr	Ala	Cys	Leu	Val	Leu	Asn
27	65					70				75					80	
28	Leu	Phe	Cys	Ala	Asp	Leu	Leu	Phe	Ile	Ser	Ala	Ile	Pro	Leu	Val	Leu
29				85					90						95	
30	Ala	Val	Arg	Trp	Thr	Glu	Ala	Trp	Leu	Leu	Gly	Pro	Val	Ala	Cys	His
31				100					105					110		
32	Leu	Leu	Phe	Tyr	Val	Met	Thr	Leu	Ser	Gly	Ser	Val	Thr	Ile	Leu	Thr
33			115					120					125			
34	Leu	Ala	Ala	Val	Ser	Leu	Glu	Arg	Met	Val	Cys	Ile	Val	His	Leu	Gln
35	130						135					140				
36	Arg	Gly	Val	Arg	Gly	Pro	Gly	Arg	Arg	Ala	Arg	Ala	Val	Leu	Leu	Ala
37	145					150					155				160	
38	Leu	Ile	Trp	Gly	Tyr	Ser	Ala	Val	Ala	Ala	Leu	Pro	Leu	Cys	Val	Phe
39				165					170					175		
40	Phe	Arg	Val	Val	Pro	Gln	Arg	Leu	Pro	Gly	Ala	Asp	Gln	Glu	Ile	Ser
41			180					185						190		
42	Ile	Cys	Thr	Leu	Ile	Trp	Pro	Thr	Ile	Pro	Gly	Glu	Ile	Ser	Trp	Asp
43			195				200					205				
44	Val	Ser	Phe	Val	Thr	Leu	Asn	Phe	Leu	Val	Pro	Gly	Leu	Val	Ile	Val

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45          210          215          220
46   Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
47   225          230          235          240
48   Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
49          245          250          255
50   Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Leu Met Val Ser
51          260          265          270
52   Phe Phe Ile Met Trp Ser Pro Ile Ile Thr Ile Leu Leu Ile Leu
53          275          280          285
54   Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
55          290          295          300
56   Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
57          305          310          315
58   Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
59          325          330          335
60   Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
61          340          345          350
62   Arg Asn Asp Leu Ser Ile Ile Ser Gly
63          355          360
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 1743
67 <212> TYPE: DNA
68 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 2
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71   gcgggcagcg ggcgacgcgc ccttgcgcag cctggagcaa gccaacgcga cccgctttcc 120
72   cttcttctcc gacgtcaagg gcgaccaccg gctggtgctg gccgcggtgg agacaaccgt 180
73   gctggtgctc atctttgcag tgctcgtcgt gggcaacgtg tgcgcctctg tctggtgtgc 240
74   gcgccgacga cgccgcgcgc cgactgcctg cctgttactc aacctcttct gcgcggacct 300
75   gctcttcacg agcgcatacc ctctggtgct ggccgtgcgc tggactgagg cctggctgct 360
76   gggccccgtt gcccgccacc tgctcttcta cgtgatgacc ctgagcgcca gcgtcaccat 420
77   cctcacgctg gccgcggtca gcctggagcg catggtgtgc atcgtgcacc tgcagcgcg 480
78   cgtgcggggt cctgggcggc gggcgcgggc agtgcgtgct gcgctcatct ggggctattc 540
79   ggcggtcgcc gctctgcctc tctgcgtctt ctttcgagtc gtcccgaac ggtcccccg 600
80   cgccgaccag gaaatttcga ttgcacact gatttggccc accattcctg gagagatctc 660
81   gtgggatgtc tottttgta ctttgaactt cttggtgcca ggactggtca ttgtgatcag 720
82   ttactccaaa attttacaga tcacaaaggc atcaaaggaag aggctcacgg taagcctggc 780
83   ctactcgag agccaccaga tccgcgtgtc ccagcaggac ttccggtctc tccgcaccct 840
84   cttcctctcc atggtctcct tottcatcat gtggagcccc atcatcatca ccatcctcct 900
85   catcctgata cagaacttca agcaagacct ggtcatcttg ccgtccctct tcttctgggt 960
86   ggtggccttc acatttgcta attcagccct aaaccccatc ctctacaaca tgacactgtg 1020
87   caggaatgag tggaagaaaa ttttttgctg cttctggttc ccagaaaagg gagccatttt 1080
88   aacagacaca tctgtcaaaa gaaatgactt gtcgattatt tctggctaatt ttttctttat 1140
89   agccgagttt ctcacacctg gcgagctgtg gcatgctttt aaacagagtt catttccagt 1200
90   accctccatc agtgccacct gctttaagaa aatgaacctt tgcaaataga cctccacagc 1260
91   tctggtaaat taagggggtg tcaccaagtt tcataatatt ttccctttat aaaaggattt 1320
92   gttggccagg tgcagtggtt catgcctgta atccagcag tttgggaggc tgaagtgagg 1380
93   ggatcacctg aggtcaggag ttcgagacca acctgaccaa catggtgaga cccccgtctc 1440
94   tactaaaaat aaaaaaaaaa attagctggg agtggtggtg ggcacctgta atcctagcta 1500

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95      cttggggaggc tgaaccagga gaatctcttg aacctgggag gcagaggttg cagtgagccg 1560
96      agatcgtgcc attgcactcc aaccagggca acaagagtga aactccatct taaaaaaaaa 1620
97      aaaaaaaaaa ttgttatgg gttcctttta aatgtgaact ttttagtggt gtttgaata 1680
98      tgatcaaatt taataaatat ttatttatga ctgttcagca aaaaaaaaaa aaaaaaaggg 1740
99      cgg 1743
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102 <211> LENGTH: 259
103 <212> TYPE: PRT
104 <213> ORGANISM: Unknown
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Description of Unknown Organism: Seven
107      Transmembrane Segment Rhodopsin Superfamily
108 <400> SEQUENCE: 3
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112           20             25             30
113      Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
114           35             40             45
115      Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
116           50             55             60
117      Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
118           65             70             75             80
119      Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
120           85             90             95
121      Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
122           100            105            110
123      Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
124           115            120            125
125      Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
126           130            135            140
127      Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
128           145            150            155            160
129      Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
130           165            170            175
131      Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
132           180            185            190
133      Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Phe Val Leu Cys
134           195            200            205
135      Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
136           210            215            220
137      Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
138           225            230            235            240
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140           245            250            255
141      Ile Ile Tyr
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 361
145 <212> TYPE: PRT

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146 <213> ORGANISM: Murine ortholog

147 <400> SEQUENCE: 4

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152   Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
153               35              40              45
154   Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
155       50              55              60
156   Val Ala Arg Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn
157       65              70              75              80
158   Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
159               85              90              95
160   Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
161               100             105             110
162   Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
163               115             120             125
164   Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
165               130             135             140
166   Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
167       145             150             155             160
168   Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu
169               165             170             175
170   Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
171               180             185             190
172   Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
173               195             200             205
174   Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
175               210             215             220
176   Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
177       225             230             235             240
178   Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
179               245             250             255
180   Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
181               260             265             270
182   Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
183               275             280             285
184   Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
185       290             295             300
186   Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
187       305             310             315             320
188   Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
189               325             330             335
190   Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
191               340             345             350
192   Arg Asn Asp Leu Ser Val Ile Ser Ser
193       355             360
195 <210> SEQ ID NO: 5

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196 <211> LENGTH: 1560
197 <212> TYPE: DNA
198 <213> ORGANISM: Murine ortholog
199 <400> SEQUENCE: 5
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202   tcgatgaccc tcttgacagc cagcagcgcg cgcagctccg ccatcttccc ggaacgctgg 180
203   gccggggcgc cggcatgtcc cctgagtgtg cacagacgac gggccctggt ccctgcgaca 240
204   cccctggacca agtcaatcgc acccaactcc ctttcttctc ggaagtcaag ggcgaccacc 300
205   ggttggtgtt gagcgtcgtg gagaccacgc ttctgggact catctttgtc gtctcactgc 360
206   tgggcaacgt gtgtgctcta gtgctggtgg cgcgcctgcg gcgcctgggg gcgtcagcca 420
207   gcctggtgct caacctcttc tgcgcggtat tgctcttcac cagcgccatc cctctagtgc 480
208   tcgtcgtcgc ctggactgag ccctggctgt tggggcccggt cgtctgcccac ctgctcttct 540
209   acgtgatgac aatgagcggc agcgtcacga tcctcacact ggcgcggtgc agcctggagc 600
210   gcatggtgtg catcgtgcgc ctccggcgcg gcttgagcgg cccggggcgg cggactcagg 660
211   cggcactgct ggctttcata tggggttact cggcgctcgc cgcgctgccc ctctacatct 720
212   tgttccgcgt ggtccgcgag cgccttcccg gcggggacca ggaaattccg atttgacat 780
213   tggattggcc caaccgcata ggagaaatct catgggatgt gtttttgag actttgaaat 840
214   tcctggtgcc gggactggtc attgtgatca gttactccaa aattttacag atcacgaaa 900
215   catcgcgga gaggcttacg ctgagcttgg catactctga gagccaccag atccgagtgt 960
216   cccaacaaga ctaccgactc ttccgcacgc tcttctctgt catggtttcc ttcttcatca 1020
217   tgtggagtcc catcatcatc accatcctcc toatcttgat ccaaaacttc cgcgaggacc 1080
218   tggtcactcg gccatccctt ttcttctggg tgggtggcctt cacgtttgcc aactctgccc 1140
219   taaaccocat actgtacaac atgtcgtgtg tcaggaaacga atggagggaag attttttgtc 1200
220   gcttcttttt tccagagaag ggagccatit ttacagatac gtctgtcagg cgaatgact 1260
221   tgtctgttat ttccagctaa ctagcctctg gtgccagggtg aaccacggtg tgcatgtaaa 1320
222   gggagttaac ttcaaggaaa gccaccaggt gcgcctgct ttaaaaaata ccgacttcca 1380
223   acagcaggca tctacggagc cagcaaatga aggaatgata gctcagtata aaaatatttt 1440
224   tccttaaaag aactttctat gggttccttt tgtgaacttt tttaagtgtg tttgtaatat 1500
225   gatctagtta ataaaatttt atttataacg tgttcctaca aaaaaaaaaa aaaaaaaaaa 1560
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228 <211> LENGTH: 300
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
231 <220> FEATURE:
232 <223> OTHER INFORMATION: mature polypeptide of 14273
233 <400> SEQUENCE: 6
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237               20             25             30
238   Leu Val Leu Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val
239               35             40             45
240   Ala Cys His Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr
241               50             55             60
242   Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val
243               65             70             75             80
244   His Leu Gln Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val
245               85             90             95

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VERIFICATION SUMMARY

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